

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/729,895A

Source: IFWO

Date Processed by STIC: 8/3/05

ENTERED

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**CRF Errors Edited by the STIC Systems
Branch**

Serial Number: 10/729,895A

CRF Edit Date: 8/8/05
Edited by: h

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

/ Deleted: ___ invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:

Revised 09/09/2003



IFWO

RAW SEQUENCE LISTING

DATE: 08/08/2005

PATENT APPLICATION: US/10/729,895A

TIME: 10:52:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082005\J729895A.raw

3 <110> APPLICANT: UNIVERSITY OF NEW MEXICO
 5 <120> TITLE OF INVENTION: OUTCOME PREDICTION AND RISK CLASSIFICATION IN CHILDHOOD
 6 LEUKEMIA
 8 <130> FILE REFERENCE: N12-038US/310.00050101
 10 <140> CURRENT APPLICATION NUMBER: 10/729,895A
 11 <141> CURRENT FILING DATE: 2003-12-05
 13 <150> PRIOR APPLICATION NUMBER: 60/510,904
 14 <151> PRIOR FILING DATE: 2003-10-14
 16 <150> PRIOR APPLICATION NUMBER: 60/510,968
 17 <151> PRIOR FILING DATE: 2003-10-14
 19 <150> PRIOR APPLICATION NUMBER: 60/432,064
 20 <151> PRIOR FILING DATE: 2002-12-06
 22 <150> PRIOR APPLICATION NUMBER: 60/432,077
 23 <151> PRIOR FILING DATE: 2002-12-06
 25 <150> PRIOR APPLICATION NUMBER: 60/432,078
 26 <151> PRIOR FILING DATE: 2002-12-06
 28 <160> NUMBER OF SEQ ID NOS: 18
 30 <170> SOFTWARE: PatentIn Ver. 3.2
 32 <210> SEQ ID NO: 1
 33 <211> LENGTH: 1080
 34 <212> TYPE: DNA
 35 <213> ORGANISM: Homo sapiens
 37 <220> FEATURE:
 38 <221> NAME/KEY: CDS
 39 <222> LOCATION: (1)..(1026)
 41 <400> SEQUENCE: 1
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 43 Met Pro Phe Leu Leu Gly Leu Arg Gln Asp Lys Glu Ala Cys Val Gly
 44 1 5 10 15
 46 acc aac aat caa agc tac atc tgt gac aca gga cac tgc tgt gga cag 96
 47 Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly His Cys Cys Gly Gln
 48 20 25 30
 50 tct cag tgc tgc aac tac tac tat gaa ctc tgg tgg ttc tgg ctg gtg 144
 51 Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp Trp Phe Trp Leu Val
 52 35 40 45
 54 tgg acc atc atc atc atc ctg agc tgc tgc tgt gtt tgc cac cac cgc 192
 55 Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys Val Cys His His Arg
 56 50 55 60
 58 cga gcc aag cac cgc ctt cag gcc cag cag cgg caa cat gaa atc aac 240
 59 Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg Gln His Glu Ile Asn
 60 65 70 75 80
 62 ctg atc gct tac cga gaa gcc cac aat tac tca gcg ctg cca ttt tat 288
 63 Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser Ala Leu Pro Phe Tyr

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Output Set: N:\CRF4\08082005\J729895A.raw

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| 64 | | 85 | | 90 | | 95 | | |
| 66 | ttc agg ttt ttg cca aac tat tta cta cct cct tat gag gaa gtg gtg | 336 | | | | | | |
| 67 | Phe Arg Phe Leu Pro Asn Tyr Leu Leu Pro Pro Tyr Glu Glu Val Val | | | | | | | |
| 68 | | 100 | | 105 | | 110 | | |
| 70 | aac cga cct cca act cct ccc cca cca tac agt gcc ttc cag cta cag | 384 | | | | | | |
| 71 | Asn Arg Pro Pro Thr Pro Pro Pro Pro Tyr Ser Ala Phe Gln Leu Gln | | | | | | | |
| 72 | | 115 | | 120 | | 125 | | |
| 74 | cag cag cag ctg ctg cct cca cag tgt ggc cct gca ggt ggc agt ccc | 432 | | | | | | |
| 75 | Gln Gln Gln Leu Leu Pro Pro Gln Cys Gly Pro Ala Gly Gly Ser Pro | | | | | | | |
| 76 | | 130 | | 135 | | 140 | | |
| 78 | ccg ggc atc gat ccc acc agg gga tcc cag ggg gca cag agc agc ccc | 480 | | | | | | |
| 79 | Pro Gly Ile Asp Pro Thr Arg Gly Ser Gln Gly Ala Gln Ser Ser Pro | | | | | | | |
| 80 | 145 | | 150 | | 155 | | 160 | |
| 82 | ttg tct gag ccc agc aga agc agc aca aga ccc cca agc atc gct gac | 528 | | | | | | |
| 83 | Leu Ser Glu Pro Ser Arg Ser Ser Thr Arg Pro Pro Ser Ile Ala Asp | | | | | | | |
| 84 | | 165 | | 170 | | 175 | | |
| 86 | cct gat ccc tct gac cta cca gtt gac cga gca gcc acc aaa gcc cca | 576 | | | | | | |
| 87 | Pro Asp Pro Ser Asp Leu Pro Val Asp Arg Ala Ala Thr Lys Ala Pro | | | | | | | |
| 88 | | 180 | | 185 | | 190 | | |
| 90 | ggg atg gag ccc agt ggc tct gtg gct ggc ctg ggg gag ctg gac ccg | 624 | | | | | | |
| 91 | Gly Met Glu Pro Ser Gly Ser Val Ala Gly Leu Gly Glu Leu Asp Pro | | | | | | | |
| 92 | | 195 | | 200 | | 205 | | |
| 94 | ggg gcc ttc ctg gac aaa gat gca gaa tgt agg gag gag ctg ctg aaa | 672 | | | | | | |
| 95 | Gly Ala Phe Leu Asp Lys Asp Ala Glu Cys Arg Glu Glu Leu Leu Lys | | | | | | | |
| 96 | | 210 | | 215 | | 220 | | |
| 98 | gat gac agc tct gaa cac ggc gca ccc gac agc aaa gag aag acg cct | 720 | | | | | | |
| 99 | Asp Asp Ser Ser Glu His Gly Ala Pro Asp Ser Lys Glu Lys Thr Pro | | | | | | | |
| 100 | 225 | | 230 | | 235 | | 240 | |
| 102 | ggg aga cat cgc cgc ttc aca ggt gac tcg ggc att gaa gtg tgt gtg | 768 | | | | | | |
| 103 | Gly Arg His Arg Arg Phe Thr Gly Asp Ser Gly Ile Glu Val Cys Val | | | | | | | |
| 104 | | 245 | | 250 | | 255 | | |
| 106 | tgc aac cgg ggc cac cat gac gat gac ctc aaa gag ttc aac aca ctc | 816 | | | | | | |
| 107 | Cys Asn Arg Gly His His Asp Asp Asp Leu Lys Glu Phe Asn Thr Leu | | | | | | | |
| 108 | | 260 | | 265 | | 270 | | |
| 110 | atc gat gat gct ctg gat ggg ccc ctg gac ttc tgc gac agc tgc cat | 864 | | | | | | |
| 111 | Ile Asp Asp Ala Leu Asp Gly Pro Leu Asp Phe Cys Asp Ser Cys His | | | | | | | |
| 112 | | 275 | | 280 | | 285 | | |
| 114 | gtg cgg ccc cct ggt gat gag gag gaa ggc ctc tgt cag tcc tct gag | 912 | | | | | | |
| 115 | Val Arg Pro Pro Gly Asp Glu Glu Glu Gly Leu Cys Gln Ser Ser Glu | | | | | | | |
| 116 | | 290 | | 295 | | 300 | | |
| 118 | gag cag gct cga gag cct ggg cac ccg cac ctg cca cgg ccg ccc gca | 960 | | | | | | |
| 119 | Glu Gln Ala Arg Glu Pro Gly His Pro His Leu Pro Arg Pro Pro Ala | | | | | | | |
| 120 | 305 | | 310 | | 315 | | 320 | |
| 122 | tgc ctg ctg ctg aac acc atc aac gag cag gac tct ccc aac tcc cag | 1008 | | | | | | |
| 123 | Cys Leu Leu Leu Asn Thr Ile Asn Glu Gln Asp Ser Pro Asn Ser Gln | | | | | | | |
| 124 | | 325 | | 330 | | 335 | | |
| 126 | agc agc agc tcc ccc agc tagagcaggt cctgccagca cccagcaact | 1056 | | | | | | |
| 127 | Ser Ser Ser Ser Pro Ser | | | | | | | |
| 128 | | 340 | | | | | | |

RAW SEQUENCE LISTING

DATE: 08/08/2005

PATENT APPLICATION: US/10/729,895A

TIME: 10:52:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082005\J729895A.raw

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130 tggcaaagca accagggtag ggga                                1080
133 <210> SEQ ID NO: 2
134 <211> LENGTH: 342
135 <212> TYPE: PRT
136 <213> ORGANISM: Homo sapiens
138 <400> SEQUENCE: 2
139 Met  Pro  Phe  Leu  Leu  Gly  Leu  Arg  Gln  Asp  Lys  Glu  Ala  Cys  Val  Gly
140   1      5      10      15
142 Thr  Asn  Asn  Gln  Ser  Tyr  Ile  Cys  Asp  Thr  Gly  His  Cys  Cys  Gly  Gln
143      20      25      30
145 Ser  Gln  Cys  Cys  Asn  Tyr  Tyr  Tyr  Glu  Leu  Trp  Trp  Phe  Trp  Leu  Val
146      35      40      45
148 Trp  Thr  Ile  Ile  Ile  Ile  Leu  Ser  Cys  Cys  Cys  Val  Cys  His  His  Arg
149      50      55      60
151 Arg  Ala  Lys  His  Arg  Leu  Gln  Ala  Gln  Gln  Arg  Gln  His  Glu  Ile  Asn
152  65      70      75      80
154 Leu  Ile  Ala  Tyr  Arg  Glu  Ala  His  Asn  Tyr  Ser  Ala  Leu  Pro  Phe  Tyr
155      85      90      95
157 Phe  Arg  Phe  Leu  Pro  Asn  Tyr  Leu  Leu  Pro  Pro  Tyr  Glu  Glu  Val  Val
158      100     105     110
160 Asn  Arg  Pro  Pro  Thr  Pro  Pro  Pro  Pro  Tyr  Ser  Ala  Phe  Gln  Leu  Gln
161      115     120     125
163 Gln  Gln  Gln  Leu  Leu  Pro  Pro  Gln  Cys  Gly  Pro  Ala  Gly  Gly  Ser  Pro
164      130     135     140
166 Pro  Gly  Ile  Asp  Pro  Thr  Arg  Gly  Ser  Gln  Gly  Ala  Gln  Ser  Ser  Pro
167 145      150     155     160
169 Leu  Ser  Glu  Pro  Ser  Arg  Ser  Ser  Thr  Arg  Pro  Pro  Ser  Ile  Ala  Asp
170      165     170     175
172 Pro  Asp  Pro  Ser  Asp  Leu  Pro  Val  Asp  Arg  Ala  Ala  Thr  Lys  Ala  Pro
173      180     185     190
175 Gly  Met  Glu  Pro  Ser  Gly  Ser  Val  Ala  Gly  Leu  Gly  Glu  Leu  Asp  Pro
176      195     200     205
178 Gly  Ala  Phe  Leu  Asp  Lys  Asp  Ala  Glu  Cys  Arg  Glu  Glu  Leu  Leu  Lys
179      210     215     220
181 Asp  Asp  Ser  Ser  Glu  His  Gly  Ala  Pro  Asp  Ser  Lys  Glu  Lys  Thr  Pro
182 225      230     235     240
184 Gly  Arg  His  Arg  Arg  Phe  Thr  Gly  Asp  Ser  Gly  Ile  Glu  Val  Cys  Val
185      245     250     255
187 Cys  Asn  Arg  Gly  His  His  Asp  Asp  Asp  Leu  Lys  Glu  Phe  Asn  Thr  Leu
188      260     265     270
190 Ile  Asp  Asp  Ala  Leu  Asp  Gly  Pro  Leu  Asp  Phe  Cys  Asp  Ser  Cys  His
191      275     280     285
193 Val  Arg  Pro  Pro  Gly  Asp  Glu  Glu  Glu  Gly  Leu  Cys  Gln  Ser  Ser  Glu
194      290     295     300
196 Glu  Gln  Ala  Arg  Glu  Pro  Gly  His  Pro  His  Leu  Pro  Arg  Pro  Pro  Ala
197 305      310     315     320
199 Cys  Leu  Leu  Leu  Asn  Thr  Ile  Asn  Glu  Gln  Asp  Ser  Pro  Asn  Ser  Gln
200      325     330     335
202 Ser  Ser  Ser  Ser  Pro  Ser

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DATE: 08/08/2005

PATENT APPLICATION: US/10/729,895A

TIME: 10:52:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082005\J729895A.raw

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203          340
207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1140
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <220> FEATURE:
213 <221> NAME/KEY: CDS
214 <222> LOCATION: (1)..(1089)
216 <400> SEQUENCE: 3
217 atg gag agg aga agg ctc ctg ggt ggc atg gcg ctc ctg ctc ctc cag 48
218 Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
219 1 5 10 15
221 gcg ctg ccc agc ccc ttg tca gcc agg gct gaa ccc ccg cag gat aag 96
222 Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
223 20 25 30
225 gaa gcc tgt gtg ggt acc aac aat caa agc tac atc tgt gac aca gga 144
226 Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
227 35 40 45
229 cac tgc tgt gga cag tct cag tgc tgc aac tac tac tat gaa ctc tgg 192
230 His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
231 50 55 60
233 tgg ttc tgg ctg gtg tgg acc atc atc atc atc ctg agc tgc tgc tgt 240
234 Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
235 65 70 75 80
237 gtt tgc cac cac cgc cga gcc aag cac cgc ctt cag gcc cag cag cgg 288
238 Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
239 85 90 95
241 caa cat gaa atc aac ctg atc gct tac cga gaa gcc cac aat tac tca 336
242 Gln His Glu Ile Asn Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser
243 100 105 110
245 gcg ctg cca ttt tat ttc agg ttt ttg cca aac tat tta cta cct cct 384
246 Ala Leu Pro Phe Tyr Phe Arg Phe Leu Pro Asn Tyr Leu Leu Pro Pro
247 115 120 125
249 tat gag gaa gtg gtg aac cga cct cca act cct ccc cca cca tac agt 432
250 Tyr Glu Glu Val Val Asn Arg Pro Pro Thr Pro Pro Pro Tyr Ser
251 130 135 140
253 gcc ttc cag cta cag cag cag cag ctg ctg cct cca cag tgt ggc cct 480
254 Ala Phe Gln Leu Gln Gln Gln Gln Leu Leu Pro Pro Gln Cys Gly Pro
255 145 150 155 160
257 gca ggt ggc agt ccc ccg ggc atc gat ccc acc agg gga tcc cag ggg 528
258 Ala Gly Gly Ser Pro Pro Gly Ile Asp Pro Thr Arg Gly Ser Gln Gly
259 165 170 175
261 gca cag agc agc ccc ttg tct gag ccc agc aga agc agc aca aga ccc 576
262 Ala Gln Ser Ser Pro Leu Ser Glu Pro Ser Arg Ser Ser Thr Arg Pro
263 180 185 190
265 cca agc atc gct gac cct gat ccc tct gac cta cca gtt gac cga gca 624
266 Pro Ser Ile Ala Asp Pro Asp Pro Ser Asp Leu Pro Val Asp Arg Ala
267 195 200 205
269 gcc acc aaa gcc cca ggg atg gag ccc agt ggc tct gtg gct ggc ctg 672

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RAW SEQUENCE LISTING

DATE: 08/08/2005

PATENT APPLICATION: US/10/729,895A

TIME: 10:52:14

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082005\J729895A.raw

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270 Ala Thr Lys Ala Pro Gly Met Glu Pro Ser Gly Ser Val Ala Gly Leu
271      210      215      220
273 ggg gag ctg gac ccg ggg gcc ttc ctg gac aaa gat gca gaa tgt agg      720
274 Gly Glu Leu Asp Pro Gly Ala Phe Leu Asp Lys Asp Ala Glu Cys Arg
275 225      230      235      240
277 gag gag ctg ctg aaa gat gac agc tct gaa cac ggc gca ccc gac agc      768
278 Glu Glu Leu Leu Lys Asp Asp Ser Ser Glu His Gly Ala Pro Asp Ser
279      245      250      255
281 aaa gag aag acg cct ggg aga cat cgc cgc ttc aca ggt gac tcg ggc      816
282 Lys Glu Lys Thr Pro Gly Arg His Arg Arg Phe Thr Gly Asp Ser Gly
283      260      265      270
285 att gaa gtg tgt gtg tgc aac cgg ggc cac cat gac gat gac ctc aaa      864
286 Ile Glu Val Cys Val Cys Asn Arg Gly His His Asp Asp Asp Leu Lys
287      275      280      285
289 gag ttc aac aca ctc atc gat gat gct ctg gat ggg ccc ctg gac ttc      912
290 Glu Phe Asn Thr Leu Ile Asp Asp Ala Leu Asp Gly Pro Leu Asp Phe
291      290      295      300
293 tgc gac agc tgc cat gtg cgg ccc cct ggt gat gag gag gaa ggc ctc      960
294 Cys Asp Ser Cys His Val Arg Pro Pro Gly Asp Glu Glu Glu Gly Leu
295 305      310      315      320
297 tgt cag tcc tct gag gag cag gct cga gag cct ggg cac ccg cac ctg      1008
298 Cys Gln Ser Ser Glu Glu Gln Ala Arg Glu Pro Gly His Pro His Leu
299      325      330      335
301 cca cgg ccg ccc gca tgc ctg ctg ctg aac acc atc aac gag cag gac      1056
302 Pro Arg Pro Pro Ala Cys Leu Leu Leu Asn Thr Ile Asn Glu Gln Asp
303      340      345      350
305 tct ccc aac tcc cag agc agc agc tcc ccc agc tagagcaggt cctgccagca 1109
306 Ser Pro Asn Ser Gln Ser Ser Ser Ser Pro Ser
307      355      360
309 cccagcaact tggcaaagca accagggtag g      1140
312 <210> SEQ ID NO: 4
313 <211> LENGTH: 363
314 <212> TYPE: PRT
315 <213> ORGANISM: Homo sapiens
317 <400> SEQUENCE: 4
318 Met Glu Arg Arg Arg Leu Leu Gly Gly Met Ala Leu Leu Leu Leu Gln
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321 Ala Leu Pro Ser Pro Leu Ser Ala Arg Ala Glu Pro Pro Gln Asp Lys
322      20      25      30
324 Glu Ala Cys Val Gly Thr Asn Asn Gln Ser Tyr Ile Cys Asp Thr Gly
325      35      40      45
327 His Cys Cys Gly Gln Ser Gln Cys Cys Asn Tyr Tyr Tyr Glu Leu Trp
328      50      55      60
330 Trp Phe Trp Leu Val Trp Thr Ile Ile Ile Ile Leu Ser Cys Cys Cys
331 65      70      75      80
333 Val Cys His His Arg Arg Ala Lys His Arg Leu Gln Ala Gln Gln Arg
334      85      90      95
336 Gln His Glu Ile Asn Leu Ile Ala Tyr Arg Glu Ala His Asn Tyr Ser
337      100      105      110

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/729,895A

DATE: 08/08/2005
TIME: 10:52:15

Input Set : A:\PTO.AMC.txt
Output Set: N:\CRF4\08082005\J729895A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:17; Xaa Pos. 4

VERIFICATION SUMMARY

DATE: 08/08/2005

PATENT APPLICATION: US/10/729,895A

TIME: 10:52:15

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08082005\J729895A.raw

L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0

DESI AVAILABLE COPY

**Raw Sequence Listing before editing,
for reference only**



IFWO

RAW SEQUENCE LISTING

DATE: 08/03/2005

PATENT APPLICATION: US/10/729,895A

TIME: 14:35:17

Input Set : A:\N12-038US Seg Listing.txt

Output Set: N:\CRF4\08032005\J729895A.raw

3 <110> APPLICANT: UNIVERSITY OF NEW MEXICO
 5 <120> TITLE OF INVENTION: OUTCOME PREDICTION AND RISK CLASSIFICATION IN CHILDHOOD
 6 LEUKEMIA
 8 <130> FILE REFERENCE: N12-038US/310.00050101
 10 <140> CURRENT APPLICATION NUMBER: 10/729,895A
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 19 <150> PRIOR APPLICATION NUMBER: 60/432,064
 20 <151> PRIOR FILING DATE: 2002-12-06
 22 <150> PRIOR APPLICATION NUMBER: 60/432,077
 23 <151> PRIOR FILING DATE: 2002-12-06
 25 <150> PRIOR APPLICATION NUMBER: 60/432,078
 26 <151> PRIOR FILING DATE: 2002-12-06
 28 <160> NUMBER OF SEQ ID NOS: 18
 30 <170> SOFTWARE: PatentIn Ver. 3.2

Does Not Comply
Corrected Diskette Needed

ERRORED SEQUENCES

628 <210> SEQ ID NO: 18
 629 <211> LENGTH: 24
 630 <212> TYPE: DNA
 631 <213> ORGANISM: Artificial Sequence
 633 <220> FEATURE:
 634 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 635 primer
 637 <400> SEQUENCE: 18
 638 tttttttttt tttttttttt tttt

24

E--> 641 12

E--> 643 12/12

VERIFICATION SUMMARY

DATE: 08/03/2005

PATENT APPLICATION: US/10/729,895A

TIME: 14:35:18

Input Set : A:\N12-038US Seg Listing.txt

Output Set: N:\CRF4\08032005\J729895A.raw

L:624 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
L:641 M:254 E: No. of Bases conflict, this line has no nucleotides.
M:254 Repeated in SeqNo=18
L:643 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:3
L:643 M:252 E: No. of Seq. differs, <211> LENGTH:Input:24 Found:25 SEQ:18